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- Homozygosity mapping and targeted genomic sequencing reveal the gene responsible for cerebellar hypoplasia and quadrupedal locomotion in a consanguineous kindred** 1995
Suleyman Gulsuner, Ayse Begum Tekinay, Katja Doerschner, Huseyin Boyaci, Kaya Bilguvar, Hilal Unal, Aslihan Ors, O. Emre Onat, Ergin Atalar, A. Nazli Basak, Haluk Topaloglu, Tulay Kansu, Meliha Tan, Uner Tan, Murat Gunel, and Tayfun Ozcelik
- Relating CNVs to transcriptome data at fine resolution: Assessment of the effect of variant size, type, and overlap with functional regions** 2004
Andreas Schlattl, Simon Anders, Sebastian M. Waszak, Wolfgang Huber, and Jan O. Korbel
- Deep-transcriptome and ribonome sequencing redefines the molecular networks of pluripotency and the extracellular space in human embryonic stem cells** 2014^{OA}
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- Epigenetic regulation of normal human mammary cell type-specific miRNAs** 2026
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Cover Human reference genomes, represented by circles; the arcs inside each circle symbolize highly related sequenced genomes (i.e., individuals from the same family or population). The colorful abstract segments on each arc show common and rare structural variation events among individual genomes. The CommonLAW package presented in this issue introduces novel combinatorial formulations and algorithms for structural variation discovery among a number of sequenced donor genomes, with the help of a complete reference genome. CommonLAW significantly reduces the false positive rate in detecting structural variation events when compared with conventional methods. (Cover illustration by Azalia Musa, modified by Andres Wanner [<http://www.pixelstorm.ch/>] and Iman Hajirasouliha, Simon Fraser University. For details, see Hormozdiari et al., pp. 2203–2212.)